



GAATCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC 39 (UPPER: SEQ ID NO.: 1)  
TTCCCTTCACTACAAACTTCAATTGCTTGGCCAAAAGAGAGTTAATTCAATGTAGACAT 19 (LOWER: SEQ ID NO.: 4)

119  
39

CTATGTAGGCAATTAAACCTATTGATGTATAAACAGTTTGCAATTCATGGAGGGCAAC 179  
59

TAAATACATTCTAGGACTTTATAAAGATCACTTTTATTATGCACAGGGTGGAACAAG 239  
79

ATGGATTATCAAGTGTCAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC 299  
M D Y Q V S S P I Y D I N Y Y T S E P C 99

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FIG. 1A-1

CAAAAATCAATGTGAAGCAAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG 359  
 Q K I N V K Q I A A R L L P P L Y S L V 119  
  
 TTCATCTTTGGTTTGTGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG 419  
 F I F G F V G N M L V I L I L I N C K R 139  
  
 CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTTCCTT 479  
 L K S M T D I Y L L N L A I S D L F F L 159  
  
 CTTACTGTCCCTTCTGGGCTCACTATGCTGCGCCCGAGTGGGACTTTGGAAATACAATG 539  
 L T V P F W A H Y A A A Q W D F G N T M 179  
  
 TGTCAACTCTTGACAGGCTCTATTTATAGGCTTCTTCTCTGGAATCTTCTTCATCATC 599  
 C Q L L T G L Y F I G F F S G I F F I I 199  
  
 CTCCTGACAAATCGATAGGTACCTGGCTGTGTCATGCTGTGTTTGCTTTAAAGCCAGG 659  
 L L T I D R Y L A V V H A V F A L K A R 219  
  
 ACGGTCACCTTTGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTGCGTCT 719  
 T V T F G V V T S V I T W V V A V F A S 239  
  
 CTCCTCAGGAATCATCTTTACCAGATCTCAAAAGAAGTCTTTCATTACACCTGCAGCTCT 779  
 L P G I I F T R S Q K E G L H Y T C S S 259  
  
 CATTTTCCATACA  
 H F P Y

FIG. 1A-2

GAATCCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGGAAGCTAGCAGCAAACC	59 (UPPER: SEQ ID NO.: 2)
	19 (LOWER: SEQ ID NO.: 5)
TTCCCTTCACTACAAAACCTTCATTGCTTGGCCAAAAGAGAGTTAATTCAATGTAGACAT	119
	39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAACAGTTTGCAATTCATGGAGGGCAAC	179
	59
TAAATACATTCTAGGACTTTATAAAAGATCACCTTTTATTATGCACAGGGTGAACAAG	239
	79
ATGGATTATCAAGTGTCAAGTCCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99

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FIG. 1B-1

CAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCTCCGCTCTACTCACTGGTG 359  
 Q K I N V K Q I A A R L L P P L Y S L V 119  
  
 TTCACTTTGGTTTGTGGCAACATGCTGGTCACTCCTCATCCTGATAAACTGCAAAAGG 419  
 F I F G F V G N M L V I L I L I N C K R 139  
  
 CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTT 479  
 L K S M T D I Y L L N L A I S D L F F L 159  
  
 CTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGGACTTTGGAAATACAATG 539  
 L T V P F W A H Y A A A Q W D F G N T M 179  
  
 TGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTCTCGGAATCTTCTTCATCATC 599  
 C Q L L T G L Y F I G F F S G I F F I I 199  
  
 CTCCTGACAAATCGATAGGTACCTGGCTGTCGTCCTCCATGCTGTGTGCTTTAAAGCCAGG 659  
 L L T I D R Y L A V V H A V F A L K A R 219  
  
 ACGGTACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTTGGCTCT 719  
 T V T F G V V T S V I T W V V A V F A S 239  
  
 CTCCTCAGGAATCATCTTTACCAGATCTCAAAAGAAGTCTTCATTACACCTGCAGCTCT 779  
 L P G I I F T R S Q K E G L H Y T C S S 259  
  
 CATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAGACATTAAAGATAGTCATC 839  
 H F P Y S Q Y Q F W K N F Q T L K I V I 279

FIG. 1B-2

TTGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCTGCTACTCGGAATCCTAAAACT 899  
 L G L V L P L L V M V I C Y S G I L K T 299  
 CTGCTTCGGTGTGAAATGAGAAGAGAGGCACAGGGCTGTGAGGCTTATCTTCACCATC 959  
 L L R C R N E K K R H R A V R L I F T I 319  
 ATGATTGTTTATTTCTCTTCTGGGCTCCCTACAACATTGTCCTTCTCCTGAACACCTTC 1019  
 M I V Y F L F W A P Y N I V L L L N T F 339  
 CAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGGTGGACCAAGCTAIGCAG 1079  
 Q E F F G L N N C S S S N R L D Q A M Q 359  
 GTGACAGAGACTCTTGGGATGACGCACCTGCTGCATCAACCCCATCATCTATGCCTTTGTC 1139  
 V T E T L G M T H C C I N P I I Y A F V 379  
 GGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCCAAAGCACATTGCCAAACGCTTC 1199  
 G E K F R N Y L L V F F Q K H I A K R F 399  
 TGCAAAATGCTGTTCTATTTCCAGCAAGAGGCTCCCGAGCGAGCAAGCTCAGTTTACACC 1259  
 C K C C S I F Q Q E A P E R A S S V Y T 419  
 CGATCCACTGGGGAGCAGGAAATACTGTGGGCTTGTGACACGGACTCAAGTGGGCTGGT 1319  
 R S T G E Q E I S V G L \* 439  
 GACCCAGTCAGAGTTGTGCACATGGGCTTAGTTTTTCATACACAGCCTGGGCTGGGGTNGG 1379  
 459  
 TTGGNNGAGGTCITTTTTTAAAGGAAGTTACTGTATTAGAGGGTCTAAGATTTCATCCATT 1439  
 479  
 TATTGGCATCTGTTTTAAAGTAGATTAGATCCGAATTC

FIG. 1B-3

GAATCCCCAACAGAGCCAAGCTCTCCATCTAGTGGACAGGAAGCTAGCAGCAAACC	59 (UPPER: SEQ ID NO. 3)
	19 (LOWER: SEQ ID NO. 6)
TTCCCTTCACTACAAACTTCATTGCTTGCCAAAAGAGAGTTAATTCATGTAGACAT	119
	39
CTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTTGCAATTCATGGAGGGCAAC	179
	59
TAAATACATTCTAGGACTTTATAAAAGATCACTTTTATTATGCACAGGGTGAACAAG	239
	79
ATGGATTATCAAGTGCAAGTCCAATCTATGACATCAATTATTATACATCGGAGCCCTGC	299
M D Y Q V S S P I Y D I N Y Y T S E P C	99

FIG. 1D-1

CAAAAAATGTAAGCAAAATCGAGCCCGCTCCTCGCTCTACTCACTGGTG 359  
 Q K I N V K Q I A A R L L P P L Y S L V 119  
 TTCATCTTTGTTTGTGGGCAACATGCTGGTCATCCTCATCCTGATAAACTGCAAAAGG 419  
 F I F G F V G N M L V I L I L I N C K R 139  
 CTGAAGAGCATGACTGACATCTACCTGCTCAACCTGGCCATCTCTGACCTGTTTTCCTT 479  
 L K S M T D I Y L L N L A I S D L F F L 159  
 CTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGGACTTTGGAATACAATG 539  
 L T V P F W A H Y A A A Q W D F G N T M 179  
 TGTCAACTCTTGACAGGGCTCTATTTATAGGCTTCTCTCGGAATCTTCTTCATCATC 599  
 C Q L L T G L Y F I G F F S G I F I I 199  
 CTCCTGACAAATCGATAGGTACCTGGCTGTCGTCATGCTGTGTTGCTTTAAAGCCAGG 659  
 L L T I D R Y L A V V H A V F A L K A R 219  
 ACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTGGTGGCTGTGTTGCGTCT 719  
 T V T F G V V T S V I T W V V A V F A S 239  
 CTCCCAGGAATCATCTTTACCAGATCTCAAAAGAGGTCTTTCATTACACCTGCAGCTCT 779  
 L P G I I F T R S Q K E G L H Y T C S S 259  
 CATTTCCATACATTAAAGATAGTCATCTTGGGGCTGGTCTGCCGCTGTTGTCAATGTT 839  
 H F P Y I K D S H L G A G P A A A C H G 279

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FIG. 1D-2

CATCTGCTACTCGGGAATCCTAA	899
899	
299	
H L L G N P K N S A S V S K *	
CAGGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTCTCTCTGCGGCTCCCTA	959
319	
CAACATTGTCTCTCCTGAAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAG	1019
339	
CTCTAACAGGTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTG	1079
359	
CATCAACCCCATCATCTATGCCTTTGTGCGGGAGAAAGTTCAGAAACTACCTCTTAGTCTT	1139
379	
CTTCCAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGC	1199
399	
TCCCCGAGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGAGCAGGAAATATCTGTGGG	1259
419	
CTTGTGACACGGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCACATGGCTTAGTT	1319
439	
TTCATACACAGCCTGGGCTGGGGTNGGTTGGNNGAGGCTTTTTTAAAGGAAGTTACT	1379
459	
GTTATAGAGGGTCTAAGATTTCATCCATTTATTGGCATCTGTTTAAAGTAGATTAGATCC	1439
479	

GAATTC

FIG. 1D-3





CCR5	YTCSSHPY	QYQF	WKNFQTLKI	V	ILGLVLP	LLVMVICYS	GILKTL	RCRNEK	KRRHRA	VLFT	IMIVYEL	FWAP	YNIVLL	LLNT	TFQEFF	GLNNC	272			
hCC-R2b	YVCGPY	FFPRG	...	WNNFHT	IMRNIL	GLVLP	LLIMVICYS	GILKTL	RCRNEK	KRRHRA	VLFT	IMIVYEL	FWTP	YNIVLL	LLNT	TFQEFF	GLSNC	280		
hCC-R3	TLCSAL	YPED	TVYSMR	HHHTIRMT	IFCLVLP	LLVMAIC	YTGIIK	TLLRCP	SKKK	YKA	RLIF	VMVFF	FWTP	YNVA	ILSS	YQSIL	FGNDC	276		
hCC-R1	HTCSL	HPHES	LRWKL	FOALK	NLFG	LVPLVMI	ICYTGIIK	ILLRRP	NEKK	SKA	VRLI	FVIMI	IFFL	FWTP	YNLT	ILSV	FDLFT	HEC	276	
hCC-R4	TYCKTK	YSLNST	TKV	VLSSE	INIL	GLVPL	IGIM	LCYSMI	IRTL	QHCK	NEKK	NKA	KMI	FAVV	VLFG	FWTP	YNIV	LELE	VQDC	279

VI

V

CCR5	SSS	NR	LDQAMQ	VTET	LG	MT	HCCIN	PII	YAFV	GKFR	NYLL	VFFQ	KHIA	KR	FKC	CSIF	QQE	APER	ASSV	YTR	ST	GE	QET	SVGL	352																			
hCC-R2b	ESTS	Q	LDQAT	QV	TET	LG	MT	HCCIN	PII	YAFV	GKFR	RYLS	VFFR	KHIT	KR	FKC	QCPV	EYRE	TV	DG	VT	STN	IP	ST	GE	QET	SVAGL	360																
hCC-R3	ERSK	H	LD	LVM	IV	TE	VI	AYSH	CC	MNP	VI	YAFV	GER	FR	KYL	RHF	FHR	LLMH	LG	RY	IP	FLP	SEK	LERT	SSV	SP	ST	AE	PET	SVF	355													
hCC-R1	EQSR	H	LD	LAV	QV	TE	VI	AYTH	CC	VNP	VI	YAFV	GER	FR	KYL	RQ	L	FRR	VAVH	LV	WLP	FL	SV	DR	L	ERV	SS	T	SP	ST	GE	HET	SVAGF	355										
hCC-R4	TFERY	LD	YAI	QAT	ET	L	AFV	HCC	LN	PII	YFF	EL	GE	KFR	KYL	IL	Q	L	FK	TC	R	GL	FV	IQ	Y	Q	GL	I	Y	S	AD	TP	SS	YT	Q	ST	MD	H	L	H	D	A	L	360

VII

FIG. 2B

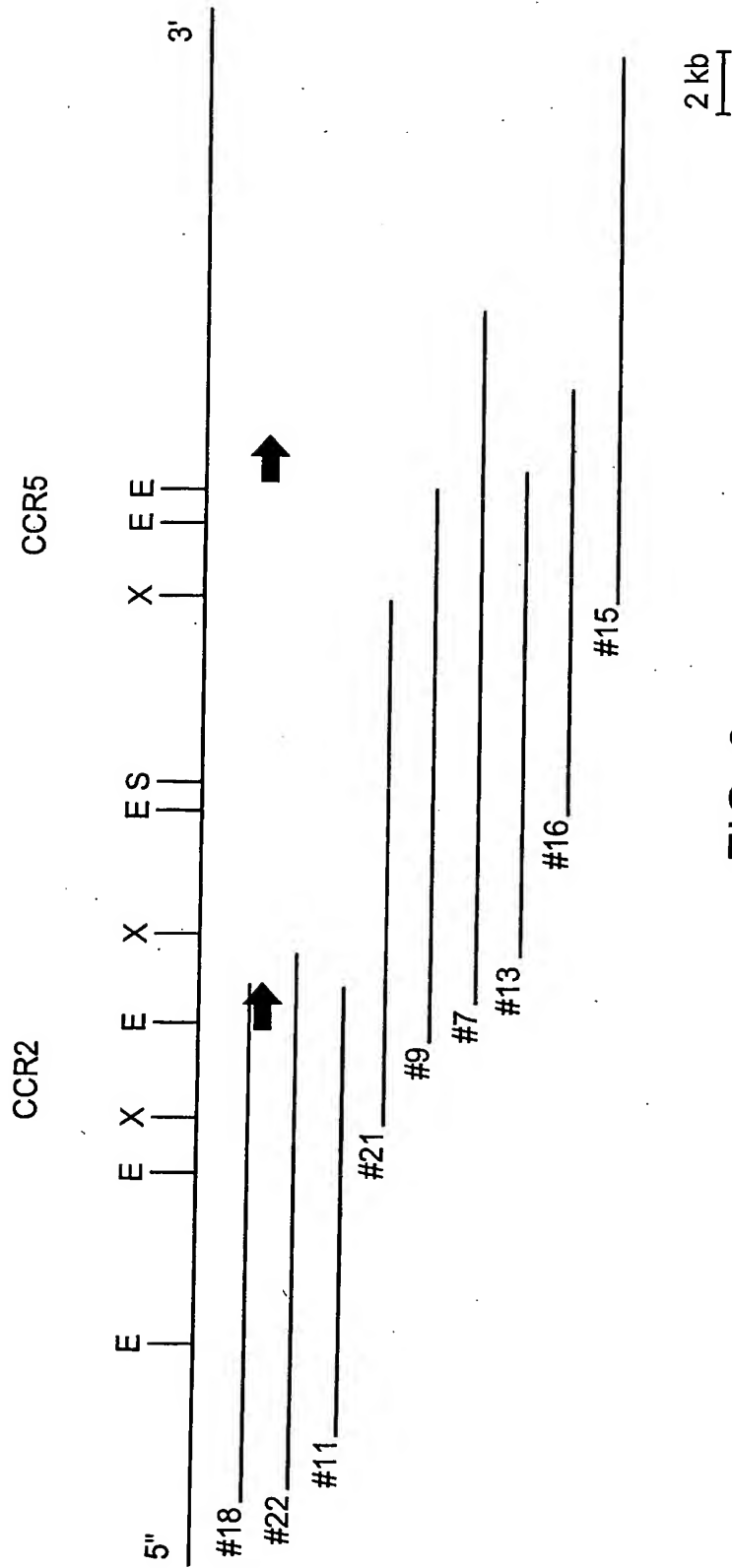


FIG. 3

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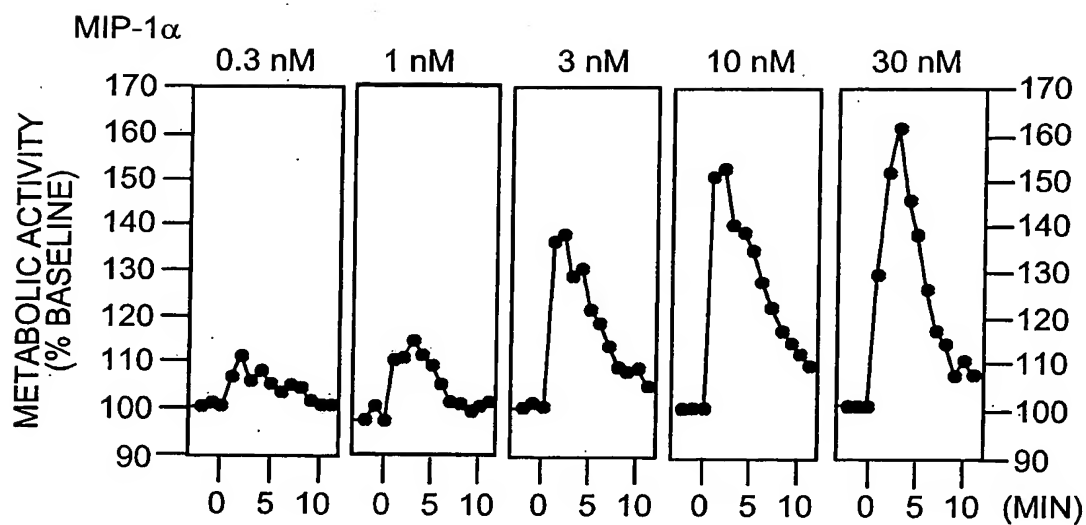


FIG. 4A

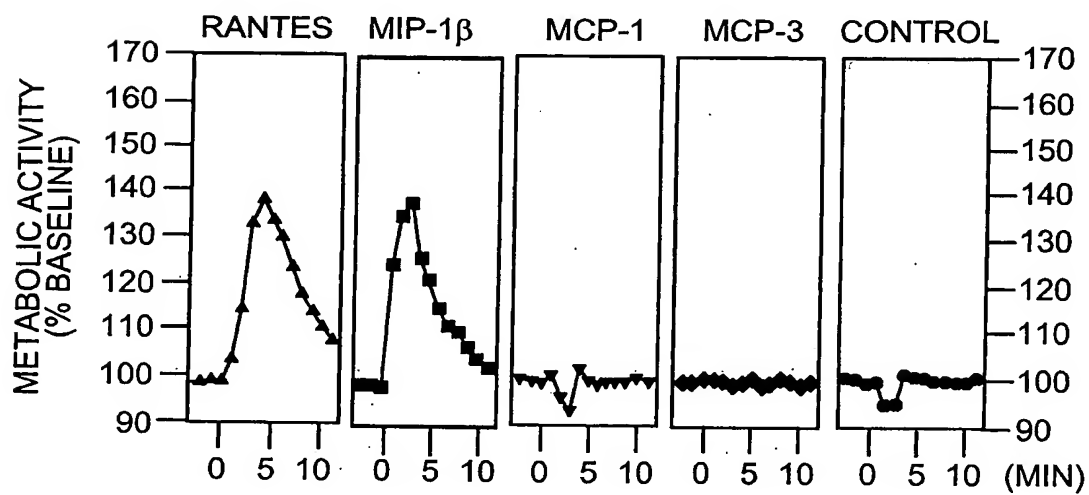


FIG. 4B

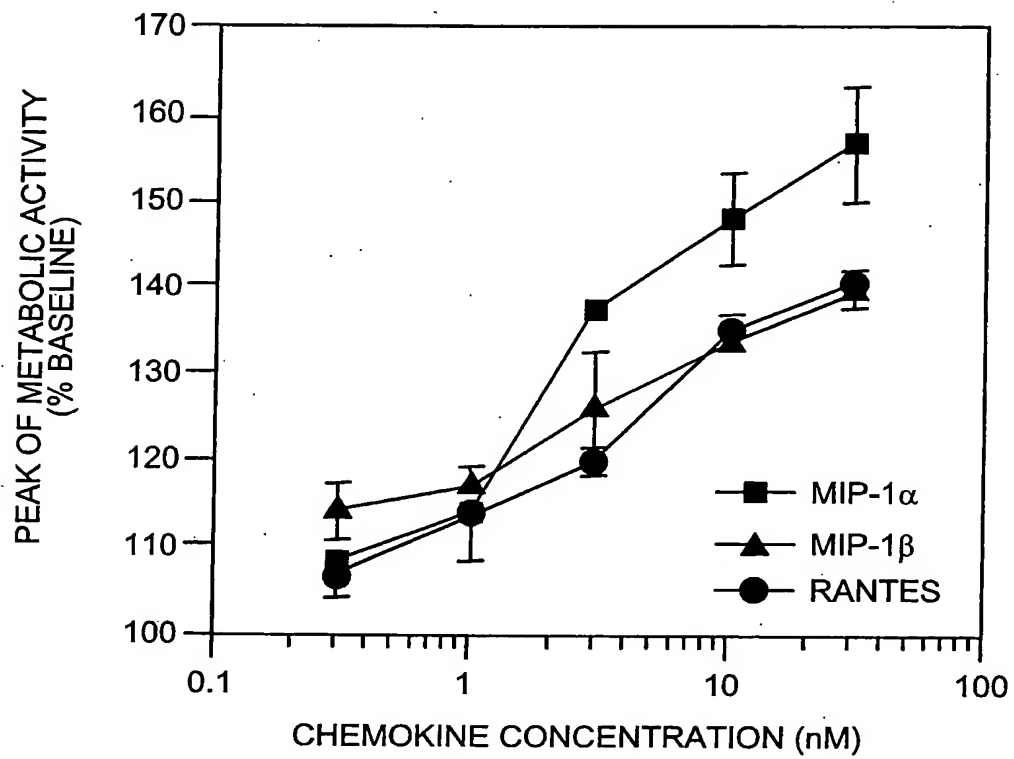


FIG. 4C

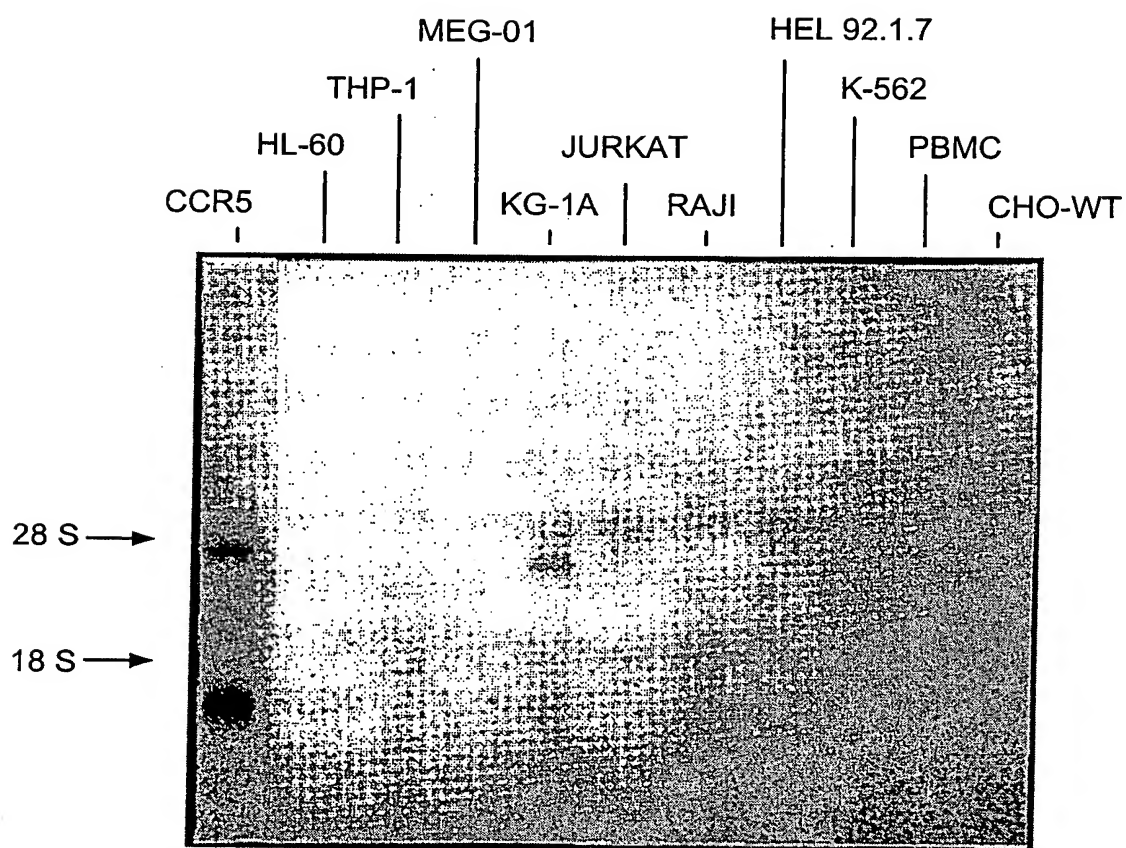


FIG. 5

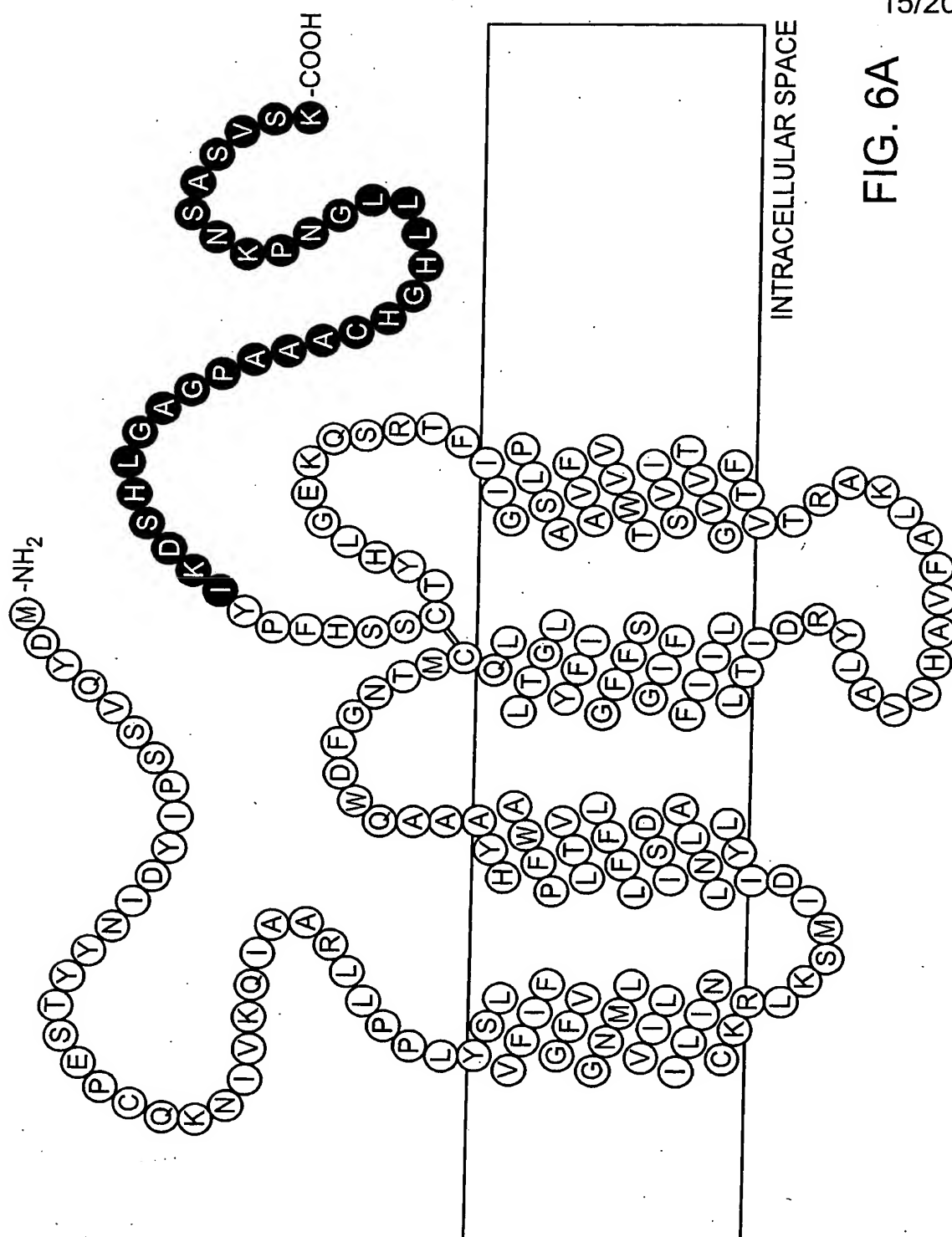


FIG. 6B



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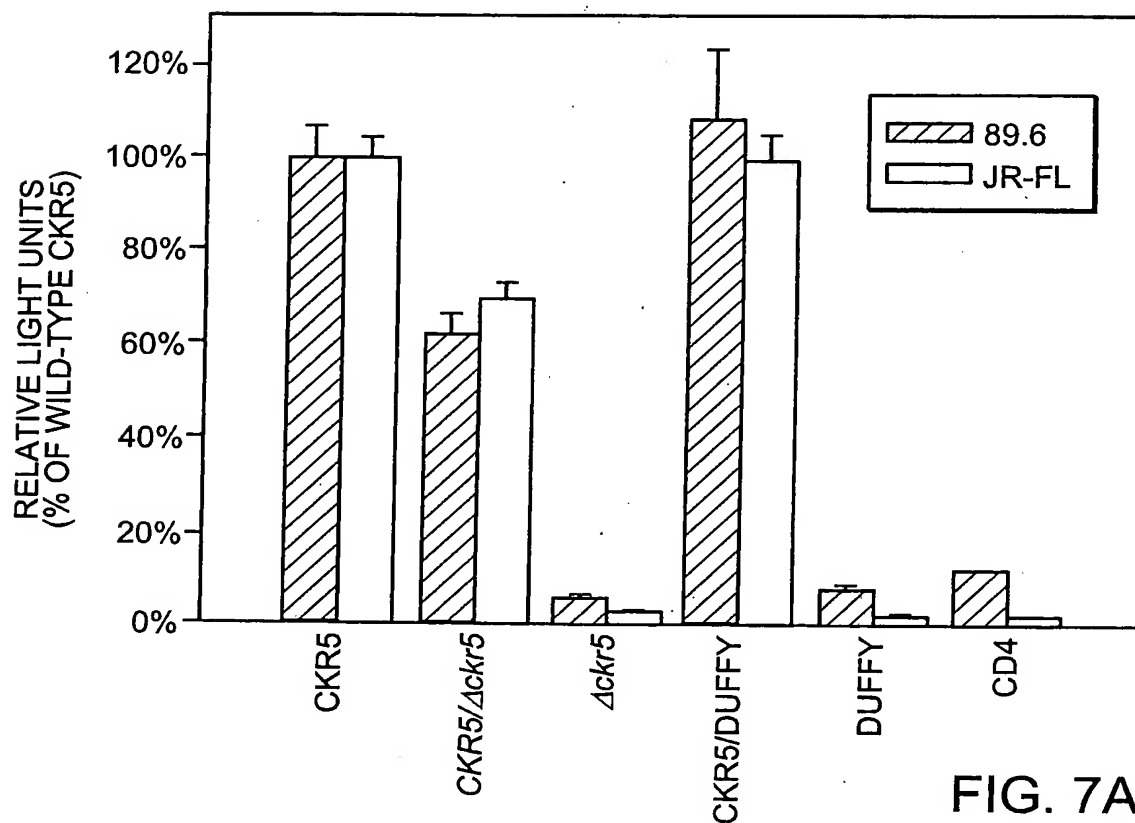


FIG. 7A

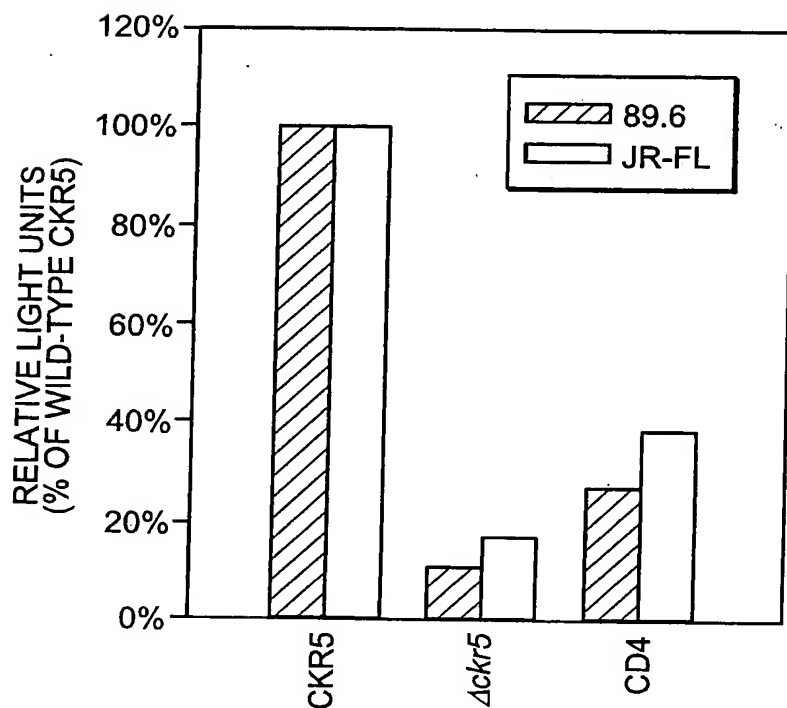


FIG. 7B

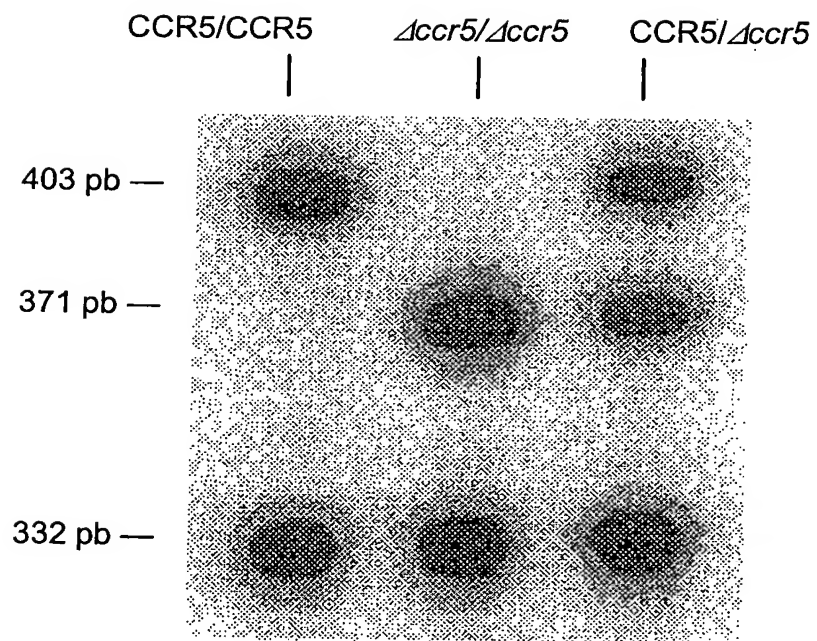


FIG. 8

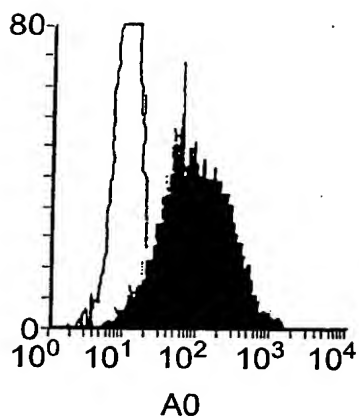


FIG. 9A

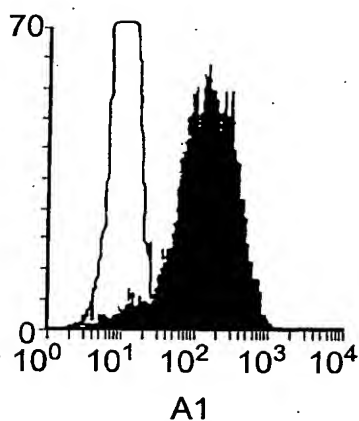


FIG. 9B

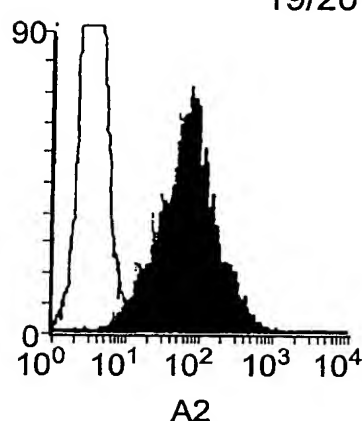


FIG. 9C

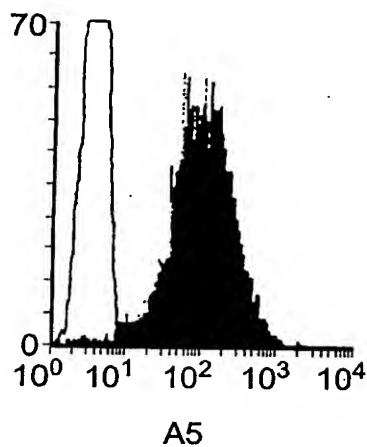


FIG. 9D

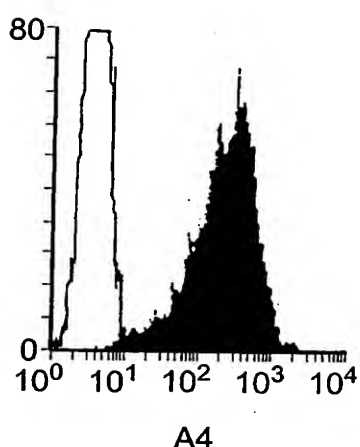


FIG. 9E

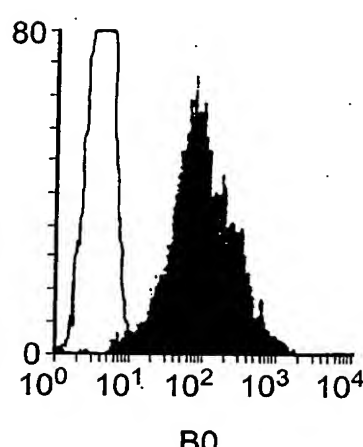


FIG. 9F

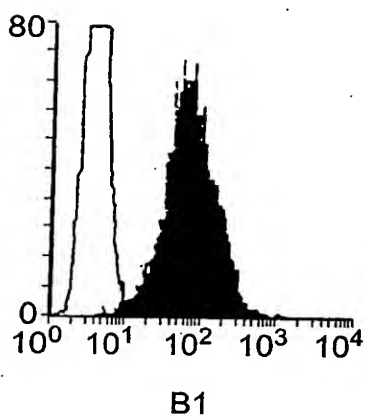


FIG. 9G

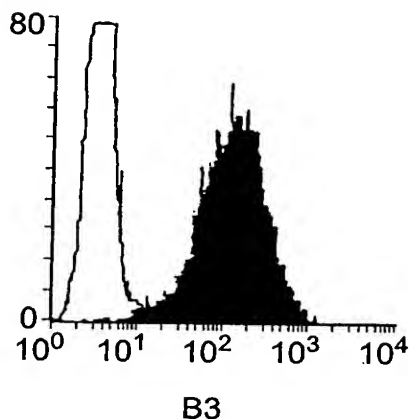


FIG. 9H

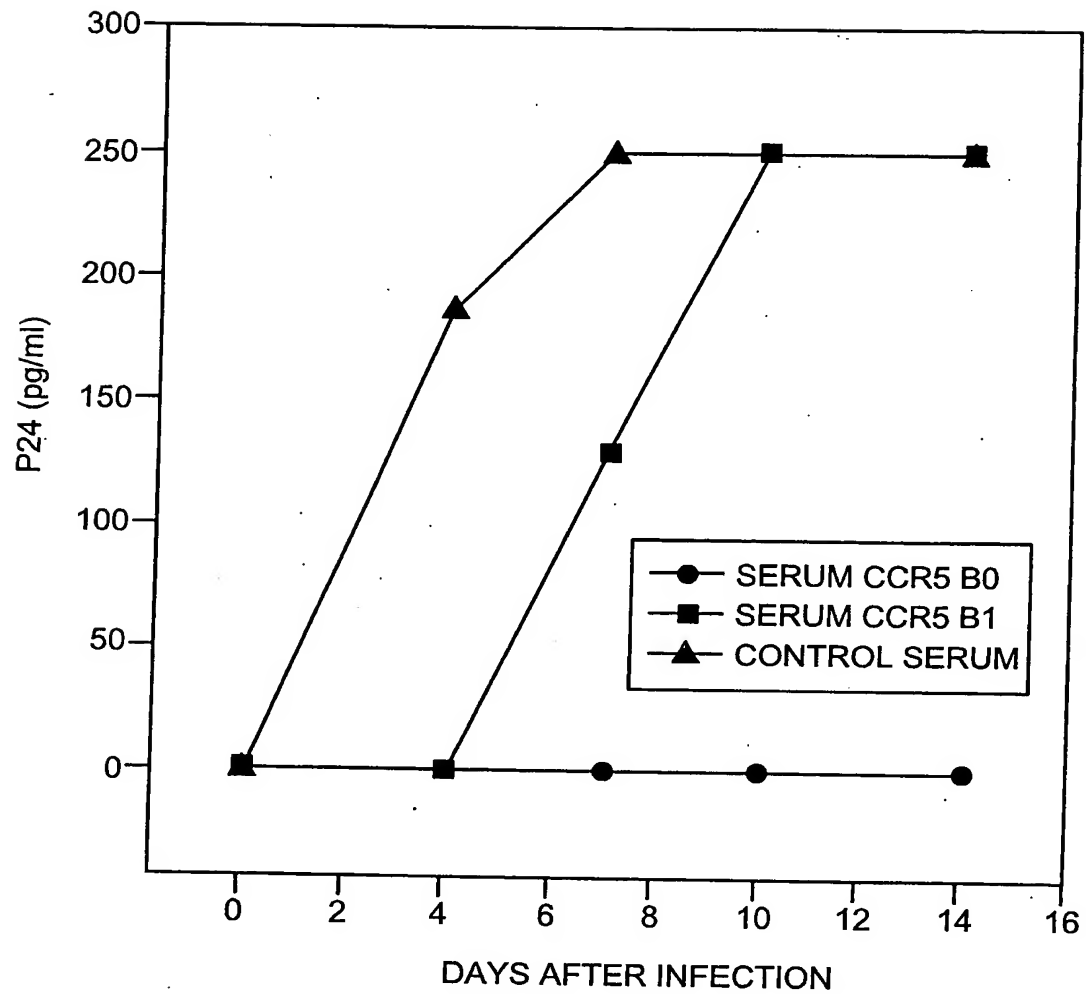


FIG. 10